## (19) World Intellectual Property Organization

International Bureau



# Rec'd FOTATT 21 DEC 2004 I COLIA CUIDIDI IN COLIDA ILIAN COLIN COLIN

#### (43) International Publication Date 15 January 2004 (15.01.2004)

**PCT** 

### (10) International Publication Number WO 2004/005479 A2

(51) International Patent Classification7:

**C12N** 

(21) International Application Number:

PCT/US2003/021153

(22) International Filing Date:

2 July 2003 (02.07.2003)

(25) Filing Language:

English

(26) Publication Language:

**English** 

(30) Priority Data: 60/393,497

2 July 2002 (02.07.2002)

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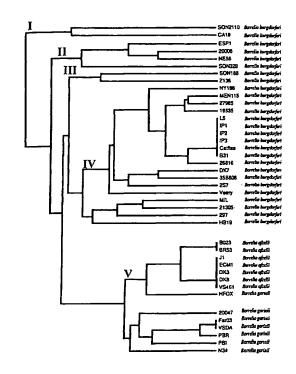
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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,

[Continued on next page]

(54) Title: A HIGH RESOLUTION TYPING SYSTEM FOR PATHOGENIC BORRELIA



VNTR Allelic Differences 0 (57) Abstract: MLVA methods for strain discrimination among globally diverseBorrelia isolates including B. burgdorferi, B. afzelii, and B. garinii are disclosed. Ten VNTR loci have been identified from genomic and plasmid sequences of Borreliastrains and primer pairs suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. The resolution of 30 unique genotypes into five to seven distinct groups is demonstrated.. This sub-typing scheme is useful for the epidemiological study of Borrelia and may be applied to the local detection of the pathological causative agent of Lyme Disease.



ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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#### Published:

 without international search report and to be republished upon receipt of that report